

Figure 1

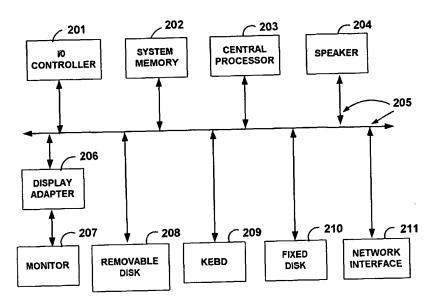


Figure 2

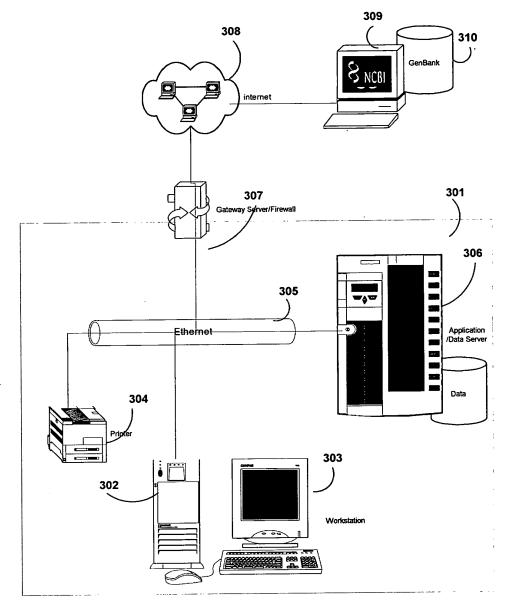


FIGURE 3

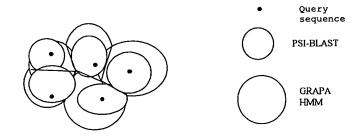


FIGURE 4

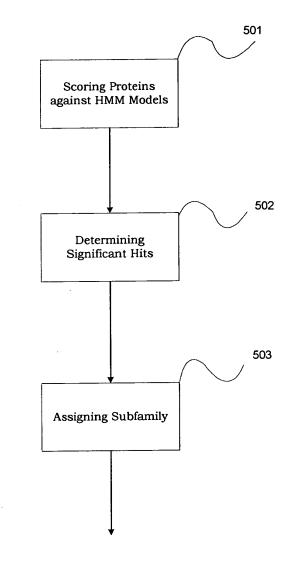
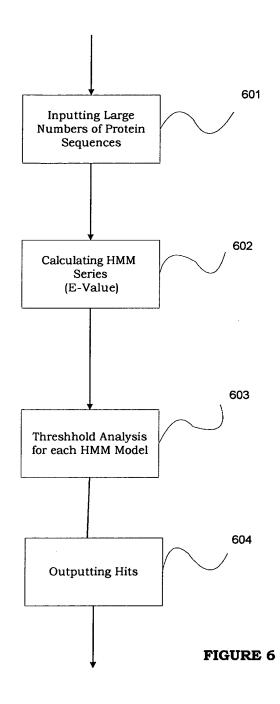


FIGURE 5



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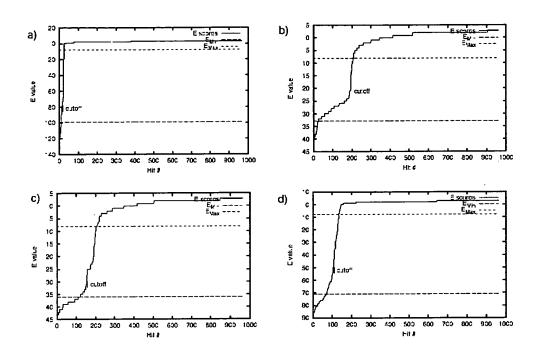
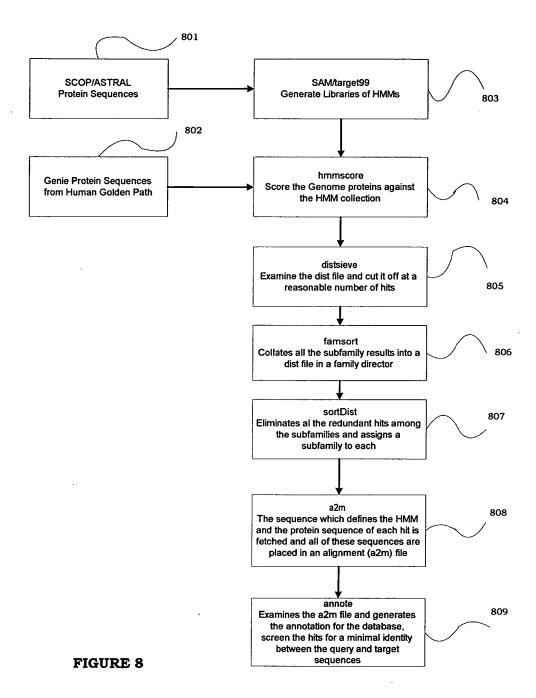


FIGURE 7



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## Alignment 1: 1>GRAPAHIT1 1 LLQDSLLRLKDYRQCFECSDVALNEAVQQMVNSGEAAAKEEWVATVTQLL 1 SVQDLNDLLSDGSGCYSLPSQPCNE VTPRIYVGNASVAQD IPKLQKL 2>1vhr 51 MGIEQALSADSSGSILKVSSSTTGLVRLTNNLIQVIDCSMAVQEEAKEPH 1>GRAPAHIT1 51 GITHVLNAAEGRSFMHVNTNAN 2>1vhr 1>GRAPAHIT1 101 VSSVLPWIILHRIIWQEEDTFHSLCHQQQLQNPAEEGMSETPMLPSSLML DSGIT 2>1vhr 1>GRAPAHIT1 151 LNTAHEYLGRRSWCCNSDGALLRFYVRVLQKELAASTSEDTHPYKEELET NDTOEFN 2>1vhr 151 YLGIKA 1>GRAPAHIT1 201 ALEQCFYCLYSFPSKKSKARYLEEHSAQQVDLIWEDALFMFEYFKPKTLP LSAYFERAA 1>GRAPAHIT1 251 EFDSYKTSTVSADLANLLKRIATIVPRTERPALSLDKVSAYIEGTSTEVP IDQALAQKNGRVL 1>GRAPAHIT1 301 CLPEGADPSPPVVNELYYLLADYHFKNKEQSKAIKFYMHDICICPNRFDS 301 C REGYSRSPTLV IAYLMMR QKMDVKSALSIVRQNREIGPN DG 2>1vhr 1>GRAPAHIT1 351 WAGMALARASRIQDKLNSNE LKS 351 F LAQLCQLNDRLAKEGKLKP 2>1vhr Alignment 2: PPADGALKRAEELKTQAN------DYFKAKDYENAIKFYSQAIE 1a17 PLCKOALEDLEKTSGHDHPDVATMLNILALVYRDQNKYKEAAHLLNDALA GRAPAHIT2 KDWKGALDAFSAVQDPHSRICFN----IGCMYTILKNMTEAEKAFTRSIN **GRAPAHIT3** L----NPSNAIYYGNRSLAYLRTECYGYALGDATR-AIELDKKYIK 1a17 IREKTLGKDHPAVAATLNNLAVLYGKRGKYKEAEPLCKR-ALEIREKVLG GRAPAHIT2 R-----DKHLAVAYFQRGMLYYQTEKYDLAIKDLKEALIQLRGNQLI **GRAPAHIT3** GYYRRAASNMA-----LG-----KFRAALRDYET-----1a17 KFHPDVAKQLSNLALLCQNQGKAEEVEYYYRRALEIYATRL----GPDDP GRAPAHIT2 DYKILGLQFKLFACEVLYNIAFMYAKKEEWKKAEEQLALATSMKSEPRHS **GRAPAHIT3** -VVKVKP-----HDKDAKMKYQECNKIVKQKAF------NVAKTKNNLASCYLKQGKYQDAETLYKEILTRAHEKEFGSVNGDNKPIWM GRAPAHIT2 GRAPAHIT3 KIDKAMECVWKQKLYEPVVIPVGKLFRPNERQVAQLAKKDYLGKATVVAS 1a17 ---ERAIA----GDEHKR-----SVVDSLDIESMTIEDEYS HAEEREES----KDKRRDSAPYGEYGSWYKACKVDSPTVNTTLR GRAPAHIT2 **GRAPAHIT3** VVDQDSFSGFAPLQPQAAEPPPRPKTPE1FRALEGEAHRVLFGFV

## FIGURE 9

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